



OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/722,544A

DATE: 03/18/2002
TIME: 15:28:22

Input Set : A:\07334-362001.txt
Output Set: N:\CRF3\03182002\I722544A.raw

Does Not Comply
Corrected Diskette Needed

3 <110> APPLICANT: Hong, Chen
4 Freimer, Nelson B.
6 <120> TITLE OF INVENTION: METHODS OF DIAGNOSING NEUROPSYCHIATRIC DISORDERS
8 <130> FILE REFERENCE: 07334-362001
10 <140> CURRENT APPLICATION NUMBER: 09/722,544A
11 <141> CURRENT FILING DATE: 2000-11-28
13 <150> PRIOR APPLICATION NUMBER: 09/236,134
14 <151> PRIOR FILING DATE: 1999-01-22
16 <150> PRIOR APPLICATION NUMBER: 60/078,044
17 <151> PRIOR FILING DATE: 1998-03-16
19 <150> PRIOR APPLICATION NUMBER: 60/088,312
20 <151> PRIOR FILING DATE: 1998-06-05
22 <150> PRIOR APPLICATION NUMBER: 60/106,056
23 <151> PRIOR FILING DATE: 1998-10-28
25 <160> NUMBER OF SEQ ID NOS: 33
27 <170> SOFTWARE: FastSEQ for Windows Version 3.0

ERRORED SEQUENCES

246 <210> SEQ ID NO: 3
247 <211> LENGTH: 1957
248 <212> TYPE: DNA
249 <213> ORGANISM: Homo sapiens
251 <220> FEATURE:
252 <221> NAME/KEY: CDS
253 <222> LOCATION: (241)...(1671)
E--> 255 <400> SEQUENCE: (13
256 tgcgtcacct gcaggcccgg gccgcggggt tggttccac cctggaggtt gctgacaccc 60
257 tgtgcctcg gctgacttcc agccgggtggc acagacgcct ccagggggca gcactcaagc 120
258 gcatctttagg aatgacagag ttgcgtccct ctckgttgcc aggctggagt tcagtggcat 180
259 gttcwtagct cactgaagcc tcaaattctt gggttcaagt gaccctccya cctcagcccc 240
260 atg agg acc tgg gac tac agt aac agc ggg aac atg aag ccg cca ctc 288
261 Met Arg Thr Trp Asp Tyr Ser Asn Ser Gly Asn Met Lys Pro Pro Leu
262 1 5 10 15
264 ttg gtg ttt att gtg tgt ctg ctg tgg ttg aaa gac agt cac tgc gca 336
265 Leu Val Phe Ile Val Cys Leu Leu Trp Leu Lys Asp Ser His Cys Ala
266 20 25 30
268 ccc act tgg aag gac aaa act gct atc agt gaa aac ctg aag agt ttt 384
269 Pro Thr Trp Lys Asp Lys Thr Ala Ile Ser Glu Asn Leu Lys Ser Phe
270 35 40 45
272 tct gag gtg ggg gag ata gat gca gat gaa gag gtg aag aag gct ttg 432
273 Ser Glu Val Gly Glu Ile Asp Ala Asp Glu Val Lys Lys Ala Leu

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274	50	55	60														
276	act	ggt	att	aag	caa	atg	aaa	atc	atg	atg	gaa	aga	aaa	gag	aag	gaa	480
277	Thr	Gly	Ile	Lys	Gln	Met	Lys	Ile	Met	Met	Glu	Arg	Lys	Glu	Lys	Glu	
278	65					70			75					80			
280	cac	acc	aat	cta	atg	agc	acc	ctg	aag	aaa	tgc	aga	gaa	gaa	aag	cag	528
281	His	Thr	Asn	Leu	Met	Ser	Thr	Leu	Lys	Lys	Cys	Arg	Glu	Glu	Lys	Gln	
282						85			90					95			
284	gag	gcc	ctg	aaa	ctt	ctg	aat	gaa	gtt	caa	gaa	cat	ctg	gag	gaa	gaa	576
285	Glu	Ala	Leu	Lys	Leu	Leu	Asn	Glu	Val	Gln	Glu	His	Leu	Glu	Glu	Glu	
286						100			105					110			
288	gaa	agg	cta	tgc	cgg	gag	tct	ttg	gca	gat	tcc	tgg	ggt	gaa	tgc	agg	624
289	Glu	Arg	Leu	Cys	Arg	Glu	Ser	Leu	Ala	Asp	Ser	Trp	Gly	Glu	Cys	Arg	
290						115			120					125			
292	tct	tgc	ctg	gaa	aat	aac	tgc	atg	aga	att	tat	aca	acc	tgc	caa	cct	672
293	Ser	Cys	Leu	Glu	Asn	Asn	Cys	Met	Arg	Ile	Tyr	Thr	Thr	Cys	Gln	Pro	
294						130			135					140			
296	agc	tgg	tcc	tct	gtg	aaa	aat	aag	att	gaa	cgg	ttt	ttc	agg	aag	ata	720
297	Ser	Trp	Ser	Ser	Val	Lys	Asn	Lys	Ile	Glu	Arg	Phe	Phe	Arg	Lys	Ile	
298						145			150					155		160	
300	tat	caa	ttt	cta	ttt	cct	ttc	cat	gaa	gat	aat	gaa	aaa	gat	ctc	ccc	768
301	Tyr	Gln	Phe	Leu	Phe	Pro	Phe	His	Glu	Asp	Asn	Glu	Lys	Asp	Leu	Pro	
302						165			170					175			
304	atc	agt	gaa	aag	ctc	att	gag	gaa	gat	gca	caa	ttg	acc	caa	atg	gag	816
305	Ile	Ser	Glu	Lys	Leu	Ile	Glu	Glu	Asp	Ala	Gln	Leu	Thr	Gln	Met	Glu	
306						180			185					190			
308	gat	gtg	ttc	agc	cag	ttg	act	gtg	gat	gtg	aat	tct	ctc	ttt	aac	agg	864
309	Asp	Val	Phe	Ser	Gln	Leu	Thr	Val	Asp	Val	Asn	Ser	Leu	Phe	Asn	Arg	
310						195			200					205			
312	agt	ttt	aac	gtc	ttc	aga	cag	atg	cag	caa	gag	ttt	gac	cag	act	ttt	912
313	Ser	Phe	Asn	Val	Phe	Arg	Gln	Met	Gln	Gln	Glu	Phe	Asp	Gln	Thr	Phe	
314						210			215					220			
316	caa	tca	cat	ttc	ata	tca	gat	aca	gac	cta	act	gag	cct	tac	ttt	ttt	960
317	Gln	Ser	His	Phe	Ile	Ser	Asp	Thr	Asp	Leu	Thr	Glu	Pro	Tyr	Phe	Phe	
318						225			230					235		240	
320	cca	gct	ttc	tct	aaa	gag	ccg	atg	aca	aaa	gca	gat	ctt	gag	caa	tgt	1008
321	Pro	Ala	Phe	Ser	Lys	Glu	Pro	Met	Thr	Lys	Ala	Asp	Leu	Glu	Gln	Cys	
322						245			250					255			
324	tgg	gac	att	ccc	aac	ttc	ttc	cag	ctg	ttt	tgt	aat	ttc	agt	gtc	tct	1056
325	Trp	Asp	Ile	Pro	Asn	Phe	Phe	Gln	Leu	Phe	Cys	Asn	Phe	Ser	Val	Ser	
326						260			265					270			
328	att	tat	gaa	agt	gtc	agt	gaa	aca	att	act	aag	atg	ctg	aag	gca	ata	1104
329	Ile	Tyr	Glu	Ser	Val	Ser	Glu	Thr	Ile	Thr	Lys	Met	Leu	Lys	Ala	Ile	
330						275			280					285			
332	gaa	gat	tta	cca	aaa	caa	gac	aaa	gct	cct	gac	cac	ggg	ctg	att		1152
333	Glu	Asp	Leu	Pro	Lys	Gln	Asp	Lys	Ala	Pro	Asp	His	Gly	Gly	Leu	Ile	
334						290			295					300			
336	tca	aag	atg	tta	cct	ggg	cag	gac	aga	gga	ctg	tgt	ggg	gaa	ctt	gac	1200
337	Ser	Lys	Met	Leu	Pro	Gly	Gln	Asp	Arg	Gly	Leu	Cys	Gly	Glu	Leu	Asp	
338						305			310					315		320	

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340	cag aat ttg tca aga tgt ttc aaa ttt cat gaa aaa tgc caa aaa tgt	1248
341	Gln Asn Leu Ser Arg Cys Phe Lys Phe His Glu Lys Cys Gln Lys Cys	
342	325 330 335	
344	cag gct cac cta tct gaa gac tgt cct gat gta cct gct ctg cac aca	1296
345	Gln Ala His Leu Ser Glu Asp Cys Pro Asp Val Pro Ala Leu His Thr	
346	340 345 350	
348	gaa tta gac gag gcg atc agg ttg gtc aat gta tcc aat cag cag tat	1344
349	Glu Leu Asp Glu Ala Ile Arg Leu Val Asn Val Ser Asn Gln Gln Tyr	
350	355 360 365	
352	ggc cag att ctc cag atg acc cgg aag cac ttg gag gac acc gcc tat	1392
353	Gly Gln Ile Leu Gln Met Thr Arg Lys His Leu Glu Asp Thr Ala Tyr	
354	370 375 380	
356	ctg gtg gag aag atg aga ggg caa ttt ggc tgg gtg tct gaa ctg gca	1440
357	Leu Val Glu Lys Met Arg Gly Gln Phe Gly Trp Val Ser Glu Leu Ala	
358	385 390 395 400	
360	aac cag gcc cca gaa aca gag atc atc ttt aat tca ata cag gta gtt	1488
361	Asn Gln Ala Pro Glu Thr Glu Ile Ile Phe Asn Ser Ile Gln Val Val	
362	405 410 415	
364	cca agg att cat gaa gga aat att tcc aaa caa gat gaa aca atg atg	1536
365	Pro Arg Ile His Glu Gly Asn Ile Ser Lys Gln Asp Glu Thr Met Met	
366	420 425 430	
368	aca gac tta agc att ctg cct tcc tct aat ttc aca ctc aag atc cct	1584
369	Thr Asp Leu Ser Ile Leu Pro Ser Ser Asn Phe Thr Leu Lys Ile Pro	
370	435 440 445	
372	ctt gaa gaa agt gct gag agt tct aac ttc att ggc tac gta gtg gca	1632
373	Leu Glu Glu Ser Ala Glu Ser Ser Asn Phe Ile Gly Tyr Val Val Ala	
374	450 455 460	
376	aaa gct cta cag cat ttt aag gaa cat ttt aaa acc tgg taagaagatc	1681
377	Lys Ala Leu Gln His Phe Lys Glu His Phe Lys Thr Trp	
378	465 470 475	
380	taatgcatcc tatatccagt aagtagaatt atctcttcat ctgggacctg gaaatcctga	1741
381	aataaaaaag gataatgcaa taaacacagt tgcaggaaag tatgttagct atatactatg	1801
382	aagtactctt agtttactta tggtaatgg cttagctatt aatactcaa ttgagttaaa	1861
383	atgaaaattc ctccttaaaa aatcaaacgt aatatgtatt acatttcatg gtacatttagt	1921
384	agttctttgt atattgaata aatactaaat caccta	1957

VERIFICATION SUMMARY
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Input Set : A:\07334-362001.txt
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L:255 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:3 differs:1
L:776 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:777 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1028 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1030 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1031 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1032 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1228 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1229 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1407 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1477 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1517 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1518 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1519 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1735 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1736 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1737 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:1738 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7